

IN THE CLAIMS:

Please note that the amended claims are shown below in clean form for clarity. A marked up version of the claim amendments is attached.

Please cancel claims 20-23, without prejudice or disclaimer. Applicants reserve the right to pursue the subject matter of these claims in one or more related applications.

Please amend claims 1 and 2 to appear as follows.

1. (Two Times Amended) A method for producing a filamentous bacterium exhibiting reduced branching and fragment septation during growth, said method comprising:

providing a filamentous bacterium, said filamentous bacterium lacking significant endogenous ssgA activity, with the capability of having or expressing heterologous SsgA-activity, which activity, in *Streptomyces griseus*, is encoded by an ssgA gene having at least the sequence:

1 ATGCGCGAGTCGGTTCAAGCAGAGGTCATGATGAGCTTCCTCGTCTCCGA
51 GGAGCTCTCGTTCGGTATTCCGGTGGAGCTCCGATACGAGGTCGGCGATC
101 CGTATGCCATCCGATGACGTTCCACCTTCCCGGCGATGCCCCCTGTGACC
151 TGGGCGTTCGGCCGCGAGCTGCTGCTGGACGGGCTCAACAGCCCGAGCGG
201 CGACGGCGATGTGCACATCGGCCCCGACCGAGCCCGAGGGCCTCGGAGATG
251 TCCACATCCGGCTCCAGGTCGGCGCGGACCGTGCGCTGTTCCGGGCGGGG
301 ACGGCACCGCTGGTGGCGTTCCTCGACGGACGGACAAGCTCGTGCCGCT
351 CGGCCAGGAGCACACGCTGGGTGACTTCGACGGCAACCTGGAGGACGCAC
401 TGGGCCGCATCCTCGCCGAGGAGCAGAACGCCGGCTGA (SEQ ID NO: 1).

2. (Two Times Amended) A method for producing a filamentous bacterium exhibiting enhanced fragmentation during growth, said method comprising:

providing a filamentous bacterium, wherein said filamentous bacterium lacks significant endogenous ssgA activity, with the capability of having or expressing heterologous ssgA-activity, which activity in *Streptomyces Griseus* is encoded by an ssgA gene having the sequence:

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cont

1 ATGCGCGAGTCGGTTCAAGCAGAGGTCATGATGAGCTTCCTCGTCTCCGA
51 GGAGCTCTCGTTCCGTATTCCGGTGGAGCTCCGATACGAGGTCGGCGATC
101 CGTATGCCATCCGGATGACGTTCCACCTTCCCGGCGATGCCCCTGTGACC
151 TGGGCGTTCGGCCGCGAGCTGCTGCTGGACGGGCTCAACAGCCCGAGCGG
201 CGACGGCGATGTGCACATCGGCCCGACCGAGCCCGAGGGCCTCGGAGATG
251 TCCACATCCGGCTCCAGGTCGGCGCGGACCGTGCCTGTTCCGGGCGGGG
301 ACGGCACCGCTGGTGGCGTTCTCGACCGGACGGACAAGCTCGTGCCGCT
351 CGGCCAGGAGCACACGCTGGGTGACTTCGACGGCAACCTGGAGGACGCAC
401 TGGGCCGCATCCTCGCCGAGGAGCAGAACGCCGGCTGA (SEQ ID NO: 1).

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